

CLAIMS

1. An isolated nucleic acid molecule comprising a sequence of nucleotides encoding or complementary to a sequence encoding a mammalian homolog of *Drosophila grh*.
2. The isolated nucleic acid molecule of claim 1 wherein the *Drosophila grh* is selected from grainyhead (*mgr*), brother of *mgr* (*bom*) and sister of *mgr* (*som*) or a mutant, derivative, homolog or analog thereof.
3. The isolated nucleic acid molecule of claim 1 wherein the nucleotide sequence of *Drosophila grh* is selected from SEQ ID NO: 17, SEQ ID NO: 34, SEQ ID NO: 36 and SEQ ID NO: 38.
4. The isolated nucleic acid molecule of claim 3 wherein the mammalian homolog comprises a nucleotide sequence having at least 65% identity after optimal alignment to one or more of SEQ ID NO: 17, SEQ ID NO: 34, SEQ ID NO: 36 and SEQ ID NO: 38 or comprises a nucleotide sequence capable of hybridizing to SEQ ID NO: 17, SEQ ID NO: 34, SEQ ID NO: 36 and/or SEQ ID NO: 38 or a complementary form thereof under stringency conditions.
5. The isolated nucleic acid molecule of claim 1 or 2 or 3 or 4 wherein the nucleic acid molecule encodes a mammalian protein transcription factor selected from human MGR p49 (SEQ ID NO: 2), human MGR p70 (SEQ ID NO: 4), human BOM (SEQ ID NO: 6), human SOM (SEQ ID NO: 7), murine MGR p61 (SEQ ID NO: 10), murine MGR p70 (SEQ ID NO: 12), murine BOM (SEQ ID NO: 14) and murine SOM (SEQ ID NO: 16).

6. An isolated nucleic acid molecule comprising a sequence of nucleotides encoding a polypeptide having transcription factor activity and comprising an amino acid sequence substantially as set forth in SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:10, SEQ ID NO:12, SEQ ID NO:14 or SEQ ID NO:16 or an amino acid sequence having at least about 60% similarity to SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:10, SEQ ID NO:12, SEQ ID NO:14 or SEQ ID NO:16 after optimal alignment wherein said polypeptide is a mammalian homolog of *Drosophila* GRH.
7. An isolated nucleic acid molecule encoding a mammalian transcription factor homolog of *Drosophila grh* and comprising a nucleotide sequence selected from SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13 and SEQ ID NO:15 or a nucleotide sequence having at least about 60% similarity to any one of SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13 or SEQ ID NO:15 after optimal alignment or a nucleotide sequence capable of hybridizing to SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13 or SEQ ID NO:15 or a complementary form thereof under low stringency conditions.
8. An isolated nucleic acid molecule comprising the nucleotide sequence set forth in SEQ ID NO: 1.
9. An isolated nucleic acid molecule comprising the nucleotide sequence set forth in SEQ ID NO: 3.
10. An isolated nucleic acid molecule comprising the nucleotide sequence set forth in SEQ ID NO: 5.
11. An isolated nucleic acid molecule comprising the nucleotide sequence set forth in SEQ ID NO: 7.

12. An isolated nucleic acid molecule comprising the nucleotide sequence set forth in SEQ ID NO: 9.
13. An isolated nucleic acid molecule comprising the nucleotide sequence set forth in SEQ ID NO: 11.
14. An isolated nucleic acid molecule comprising the nucleotide sequence set forth in SEQ ID NO: 13.
15. An isolated nucleic acid molecule comprising the nucleotide sequence set forth in SEQ ID NO: 15.
16. A method for identifying a M-GRH, said method comprising screening a nucleotide database and identifying a nucleotide sequence having at least 60% similarity to SEQ ID NO:17 or SEQ ID NO:34 or SEQ ID NO:36 or SEQ ID NO:38 after optimal alignment.
17. Means of identifying a nucleotide sequence likely to encode an M-GRH transcription factor, said method comprising interrogating a mammalian genome database conceptually translated into different reading frames with an amino acid sequence defining *Drosophila GRH* or any one of SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:10, SEQ ID NO:12, SEQ ID NO:14 and SEQ ID NO:16 and identifying a nucleotide sequence corresponding to an amino acid sequence having at least about 60% similarity to *Drosophila GRH* or to any one of SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:10, SEQ ID NO:12, SEQ ID NO:14 and SEQ ID NO:16.

18. A method for detecting an aberrant phenotype or a propensity for an aberrant phenotype to develop, said method comprising screening for a variation in a nucleotide sequence encoding a mammalian MGR, BOM and/or SOM or their homologs.
19. An isolated mammalian transcription factor which is a homolog of *Drosophila* grainyhead (GRH) selected from human MGR p49 (SEQ ID NO: 2), human MGR p70 (SEQ ID NO: 4), human BOM (SEQ ID NO: 6), human SOM (SEQ ID NO: 8), murine MGR p61 (SEQ ID NO: 10), murine MGR p70 (SEQ ID NO: 12), murine BOM (SEQ ID NO: 14) and murine SOM (SEQ ID NO: 16).
20. An antibody to be isolated transcription factor of claim 19.
21. The antibody of claim 20 wherein the antibody is a monoclonal antibody.
22. A method for detecting an aberrant phenotype or a propensity for an aberrant phenotype to develop, said method comprising screening for a variation in an amino acid sequence encoding MGR, BOM and/or SOM or their homologs.
23. A method for detecting a mammalian transcription factor or fragment thereof in a biological sample from a subject, said method comprising contacting said biological sample with an antibody specific for said mammalian transcription factor or fragment thereof or its derivatives or homologs for a time and under conditions sufficient for an antibody-polypeptide complex to form, and then detecting said complex.
24. An animal model comprising a genetically modified animal comprising a nucleotide insertion, deletion, addition and/or substitution in a nucleic acid mole of claims 1 to 15.
25. A medical assessment system comprising the animal model of claim 24.